

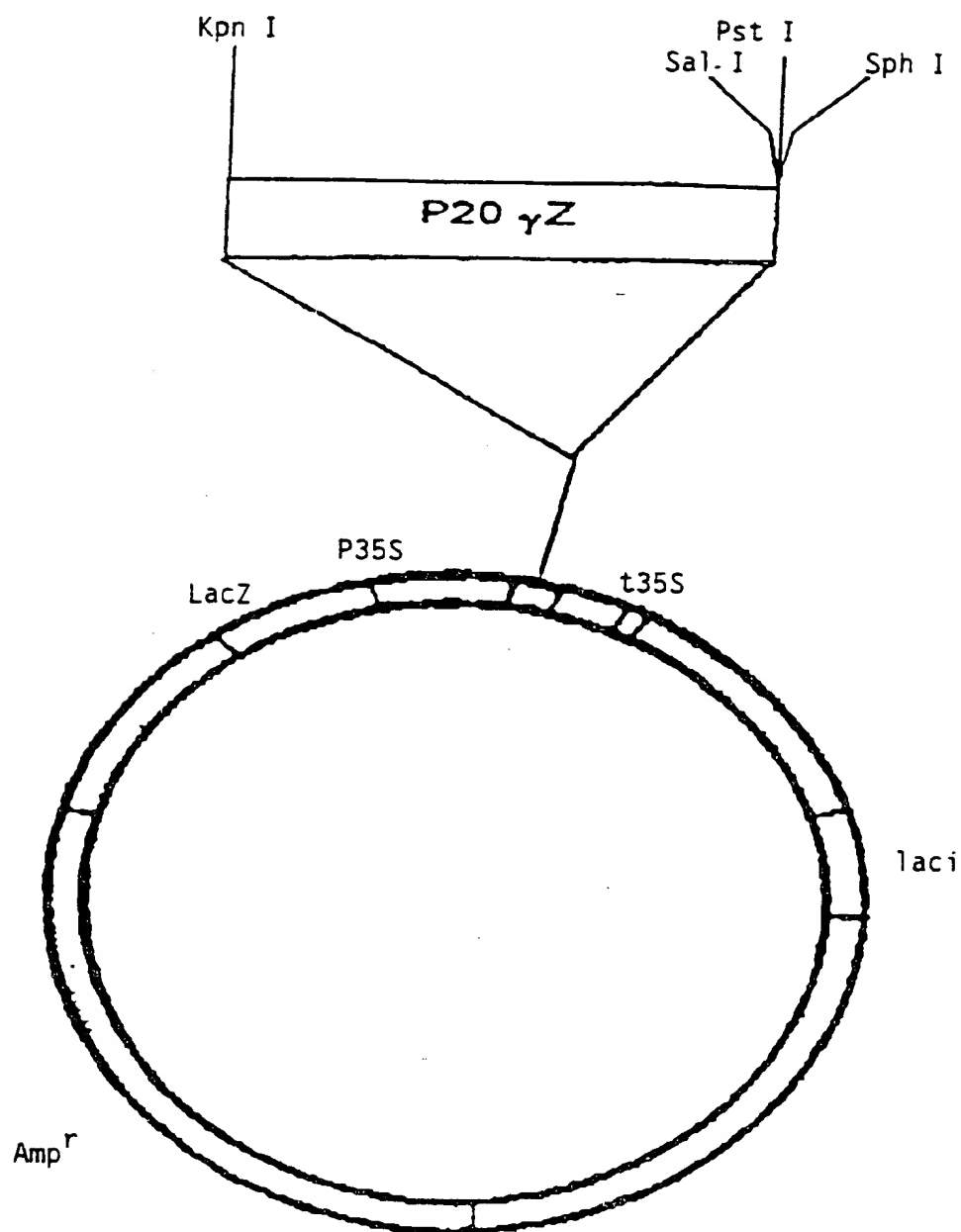
pP20 γ Z

FIGURE 1

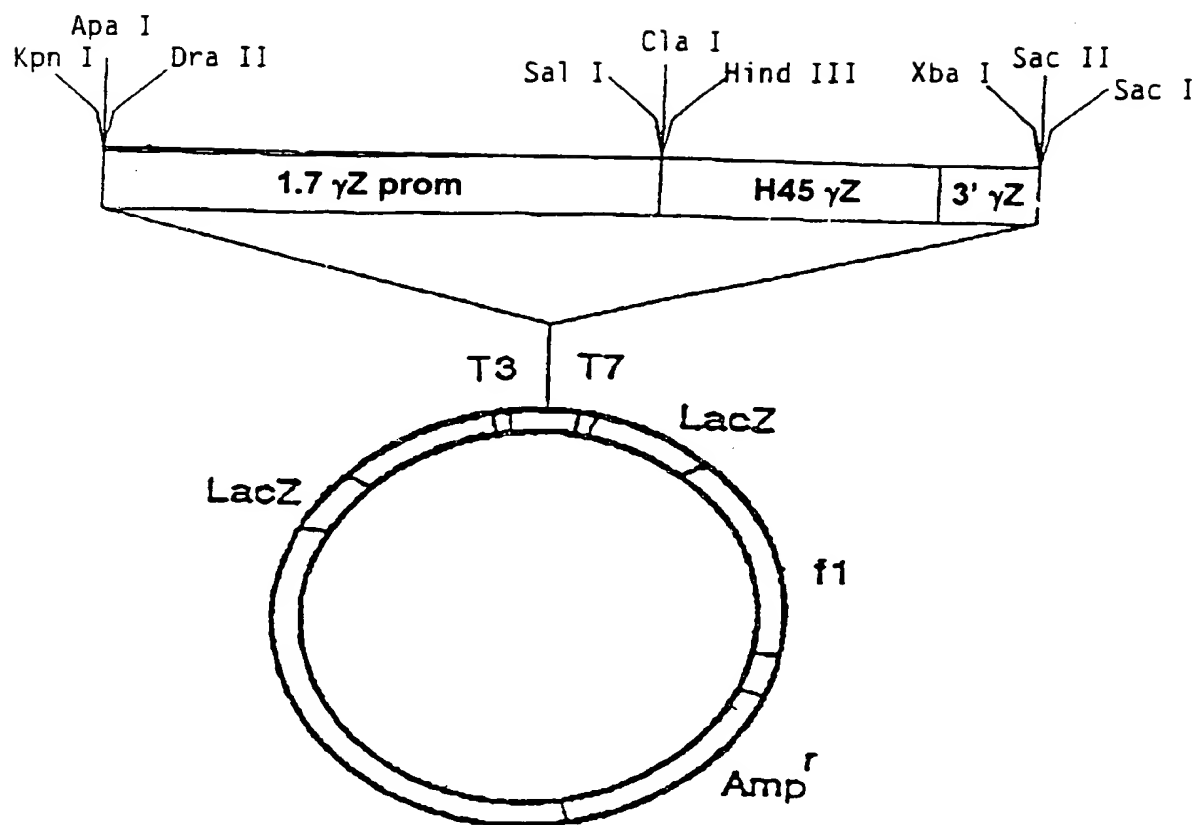
pH45 γ Z

FIGURE 2

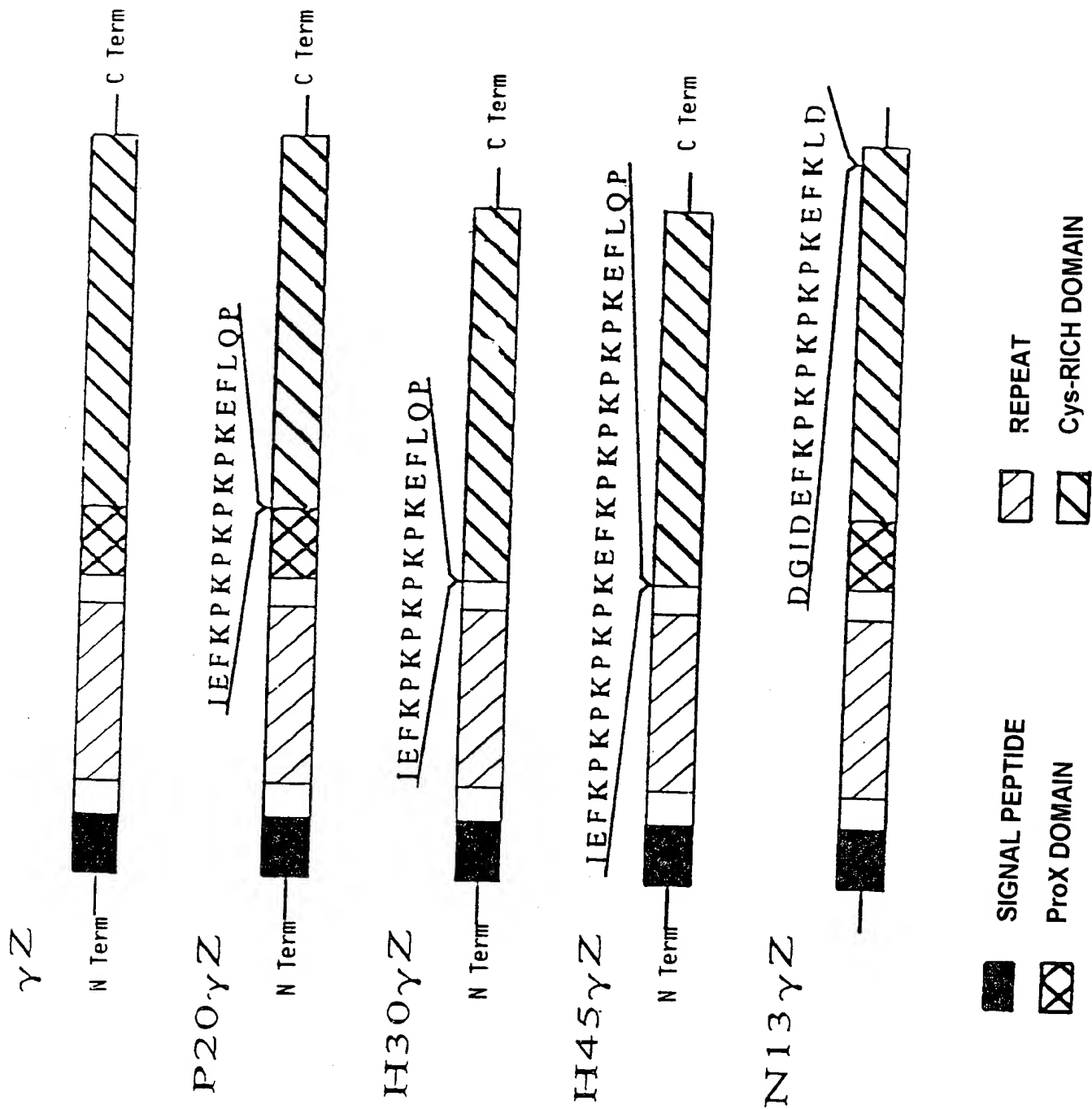


FIGURE 3

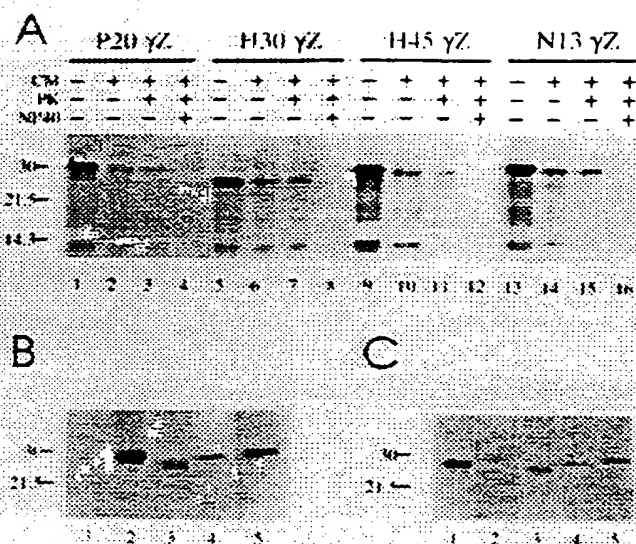


FIGURE 4

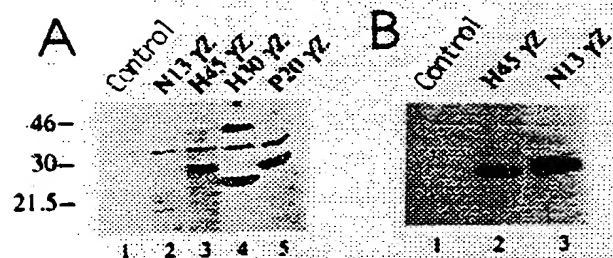


FIGURE 6

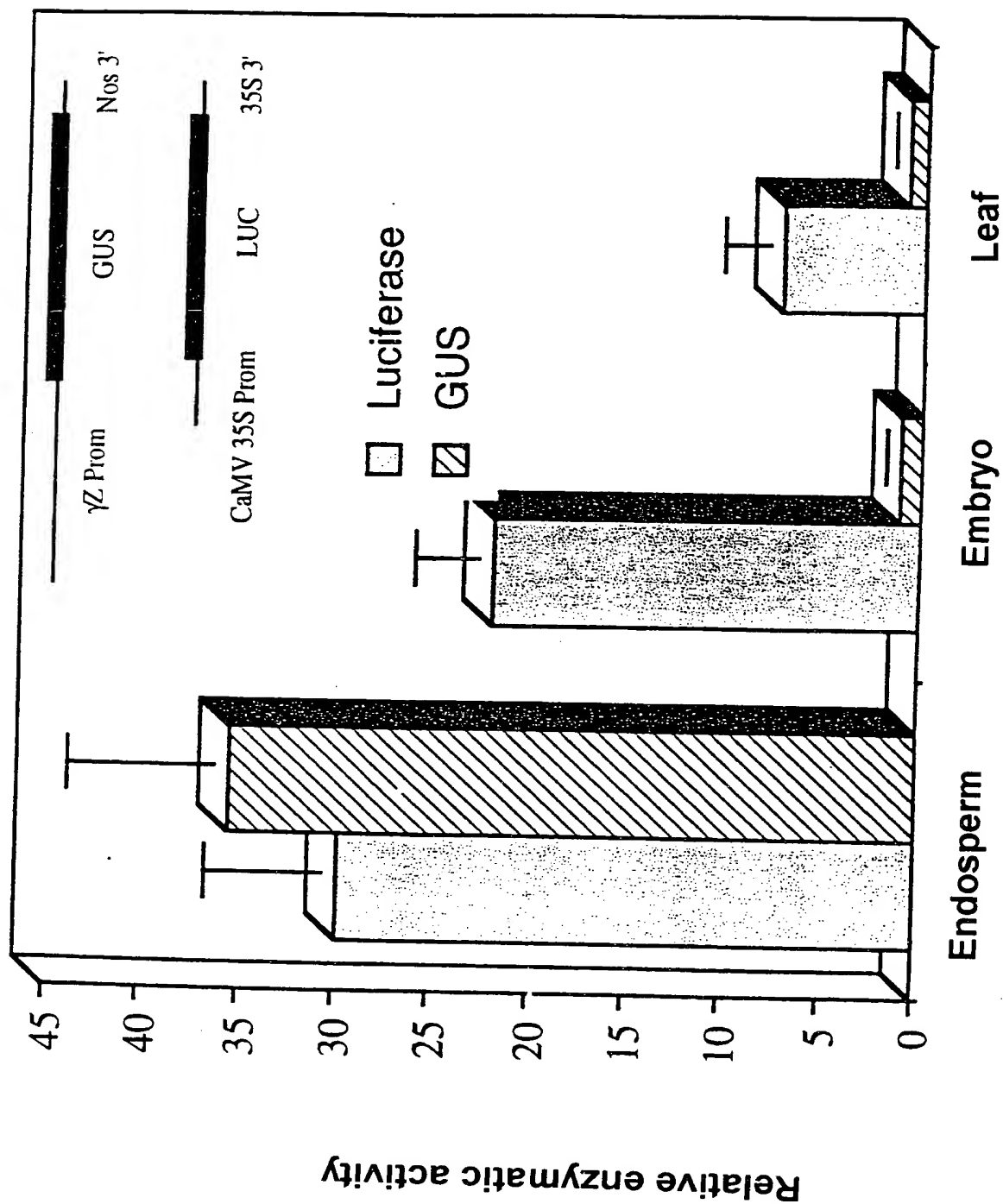


FIGURE 5

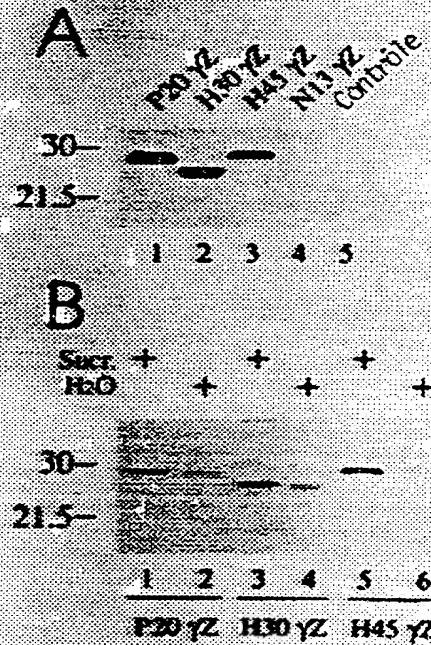


FIGURE 7

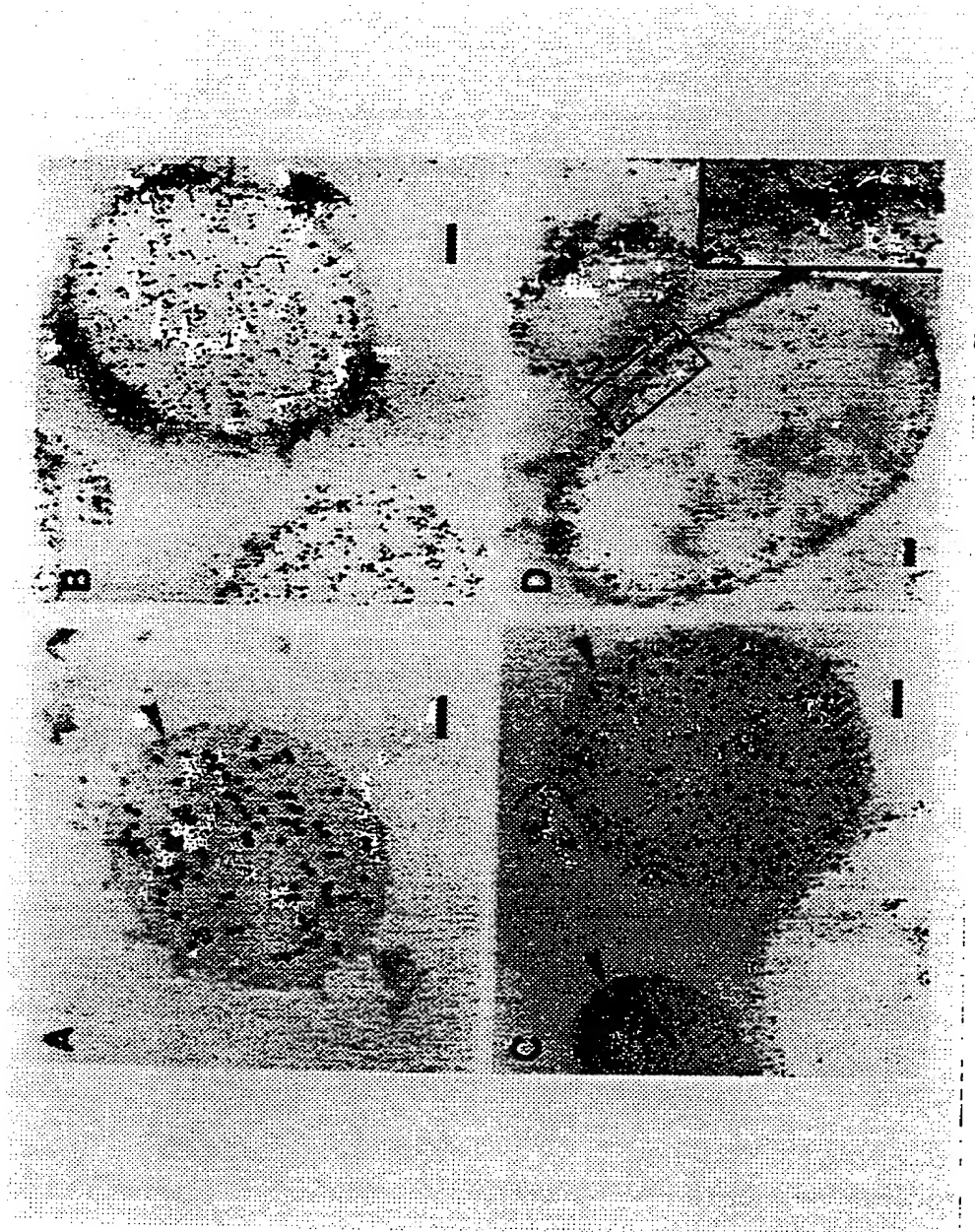


FIGURE 8

8 / 17

 γ -Zéine

10 20 30 40 50 60
| | | | |
ATGAGGGTGTGCTCGTTGCCCTCGCTCTCCTGGCTCTCGCTGCGAGCGCCACCTCCACG
M R V L L V A L A L L A L A S A T S T

70 80 90 100 110 120
| | | | |
CATACAAGCGGGCTGCGGCTGCCAGCCACCGCCGCGGTTTCATCTACCGCCGCGGCTG
H T S G G C G C Q P P P P V H L P P P V

130 140 150 160 170 180
| | | | |
CATCTGCCACCTCCGGTTCACCTGCCACCTCCGGTGCATCTCCACCGCCGGTCCACCTG
H L P P P V H L P P P V H L P P P V H L

190 200 210 220 230 240
| | | | |
CCGCCGCGGTCCACCTGCCACCGCCGGTCCATGTGCCGCGCGGTTTCATCTGCCGCGG
P P P V H L P P P V H V P P P V H L P P

250 260 270 280 290 300
| | | | |
CCACCATGCCACTACCCTACTCAACCGCCCCGGCCTCAGCCTCATCCCCAGCCACACCCA
P P C H Y P T Q P P R P Q P H P Q P H P

310 320 330 340 350 360
| | | | |
TGCCCGTGCCAAACAGCCGCATCCAAGCCCGTGCCAGCTGCAGGGAACCTGCGGCGTTGGC
C P C Q Q P H P S P C Q L Q G T C G V G

370 380 390 400 410 420
| | | | |
AGCACCCCGATCCTGGGCCAGTGCCTCGAGTTTCTGAGGCATCAGTGCAGCCCGACGGCG
S T P I L G Q C V E F L R H Q C S P T A

430 440 450 460 470 480
| | | | |
ACGCCCTACTGCTCGCCTCAGTGCCAGTCGTTGCGGCAGCAGTGTGTCAGCAGCTCAGG
T P Y C S P Q C Q S L R Q Q C C Q Q L R

490 500 510 520 530 540
| | | | |
CAGGTGGAGCCGCGAGCACCGGTACCAGGCGATCTTCGGCTTGGTCCTCCAGTCCATCCTG
Q V E P Q H R Y Q A I F G L V L Q S I L

550 560 570 580 590 600
| | | | |
CAGCAGCAGCCGCAAAGCGGCCAGGTGCGGGGCTGTTGGCGGCGCAGATAGCGCAGCAA
Q Q Q P Q S G Q V A G L L A A Q I A Q Q

FIGURE 9
REPLACEMENT PAGE (RULE 26)

610	620	630	640	650	660
CTGACGGCGATGTGCGGCCTGCAGCAGCCGACTCCATGCCCTACGCTGCTGCCGGCGGT					
L T A M C G L Q Q P T P C P Y A A A G G					

670
GTCCCCCACTGA
V P H -

FIGURE 9 (CONTINUED)

H45 γ Z

10 20 30 40 50 60
| | | | |
ATGAGGGTGTGCTCGTTGCCCTCGCTCTCCTGGCTCTCGCTGCGAGCGCCACCTCCACG
M R V L L V A L A L L A A S A T S T

70 80 90 100 110 120
| | | | |
CATAAAGCGGCGGCTGCGGCTGCCAGCCACCGCCGCGGTTCATCTACCGCCGCGCGGTG
H T S G G C G C Q P P P P V H L P P P V

130 140 150 160 170 180
| | | | |
CATCTGCCACCTCCGGTTCACCTGCCACCTCCGGTGCATCTCCCACCGCCGGTCCACCTG
H L P P P V H L P P P V H L P P P V H L

190 200 210 220 230 240
| | | | |
CCGCCGCGGTCCACCTGCCACCGCCGGTCCATGTGCCGCGCGCGGTTCATCTGCCGCCG
P P P V H L P P P V H V P P P V H L P P

250 260 270 280 290 300
| | | | |
CCACCATGCCACTACCCTACTCAACCGCCCCGGATCGAATTCAAACCAAAGCCAAAGCCG
P P C H Y P T Q P P R I E F K P K P K P

310 320 330 340 350 360
| | | | |
AAGCCAAAAGAATTCAAACCAAAGCCAAAGCCGAAGCCAAAAGAATTCCTGCAGCCCCTG
K P K E F K P K P K P K P K E F L Q P L

370 380 390 400 410 420
| | | | |
CAGGGAACCTGCGGCGTTGGCAGCACCCCGATCCTGGGCCAGTGCGTTCGAGTTTCTGAGG
Q G T C G V G S T P I L G Q C V E F L R

430 440 450 460 470 480
| | | | |
CATCAGTGCGAGCCCGACGGCGACGCCCTACTGCTCGCCTCAGTGCCAGTCGTTGCGGCAG
H Q C S P T A T P Y C S P Q C Q S L R Q

490 500 510 520 530 540
| | | | |
CAGTGTTGCCAGCAGCTCAGGCAGGTGGAGCCGCAGCACCGGTACCAGGCGATCTTCGGC
Q C C Q Q L R Q V E P Q H R Y Q A I F G

550 560 570 580 590 600
| | | | |
TTGGTCCTCCAGTCCATCCTGCAGCAGCAGCCGCAAAGCGGCCAGGTGCGGGGCTGTTG
L V L Q S I L Q Q Q P Q S G Q V A G L L

610 620 630 640 650 660
| | | | |
GCGGCGCAGATAGCGCAGCAACTGACGGCGATGTGCGGCCTGCAGCAGCCGACTCCATGC
A A Q I A Q Q L T A M C G L Q Q P T P C

FIGURE 10

			670					680					690				
C	C	T	A	C	G	C	T	G	C	C	G	G	C	G	T	G	T
C	C	C	T	A	C	G	C	T	G	C	C	G	G	C	G	T	G
C	C	C	C	C	C	C	C	A	C	T	G	A					
P	Y	A	A	A	G	G	V	P	H	-							

FIGURE 10 (CONTINUED)

P20 γ Z

10 20 30 40 50 60
| | | | |
ATGAGGGTGTGCTCGTTGCCCTCGCTCTCCTGGCTCTCGCTGCGAGCGCCACCTCCACG
M R V L L V A L A L L A A S A T S T

70 80 90 100 110 120
| | | | |
CATACAAGCGGCGGCTGCGGCTGCCAGCCACCGCCGCGGTTTCATCTACCGCCGCGGCTG
H T S G G C G C Q P P P P V H L P P P V

130 140 150 160 170 180
| | | | |
CATCTGCCACCTCCGGTTCACCTGCCACCTCCGGTGATCTCTCCACCGCCGGTCCACCTG
H L P P P V H L P P P V H L P P P V H L

190 200 210 220 230 240
| | | | |
CCGCGCGCGGTCCACCTGCCACCGCCGGTCCATGTGCCGCGCGCGGTTTCATCTGCCGCGG
P P P V H L P P P V H V P P P V H L P P

250 260 270 280 290 300
| | | | |
CCACCATGCCACTACCCTACTCAACCGCCCCGGCCTCAGCCTCATCCCCAGCCACACCCA
P P C H Y P T Q P P R P Q P H P Q P H P

310 320 330 340 350 360
| | | | |
TGCCCGTGCCAACAGCCGCATCCAAGCCCGTGCCAGATCGAATTCAAACCAAAGCCAAAG
C P C Q Q P H P S P C Q I E F K P K P K

370 380 390 400 410 420
| | | | |
CCGAAGCCAAAAGAATTCCTGCAGCCCCTGCAGGGAACCTGCGGCGTTGGCAGCACCCCG
P K P K E F L Q P L Q G T C G V G S T P

430 440 450 460 470 480
| | | | |
ATCCTGGGCCAGTGCCTCGAGTTTCTGAGGCATCAGTGCAGCCCGACGGCGACGCCCTAC
I L G Q C V E F L R H Q C S P T A T P Y

490 500 510 520 530 540
| | | | |
TGCTCGCCTCAGTGCCAGTCGTTGCGGCAGCAGTGTGTCAGCAGCTCAGGCAGGTGGAG
C S P Q C Q S L R Q Q C C Q Q L R Q V E

550 560 570 580 590 600
| | | | |
CCGCAGCACCGGTACCAGGCGATCTTCGGCTTGGTCCTCCAGTCCATCCTGCAGCAGCAG
P Q H R Y Q A I F G L V L Q S I L Q Q Q

610 620 630 640 650 660
| | | | |
CCGCAAAGCGGCCAGGTGCGGGGCTGTTGGCGGCGCAGATAGCGCAGCAACTGACGGCG
P Q S G Q V A G L L A A Q I A Q Q L T A

FIGURE 11

REPLACEMENT PAGE (RULE 26)

670	680	690	700	710	720														
ATGTGCGGCCTGCAGCAGCCGACTCCATGCCCCTACGCTGCTGCCGGCGGTGTCCCCAC																			
M	C	G	L	Q	Q	P	T	P	C	P	Y	A	A	A	G	G	V	P	H

TGA

-

FIGURE 11 (CONTINUED)

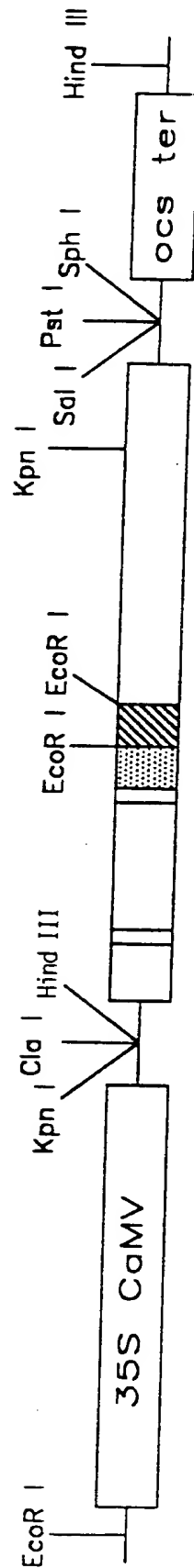
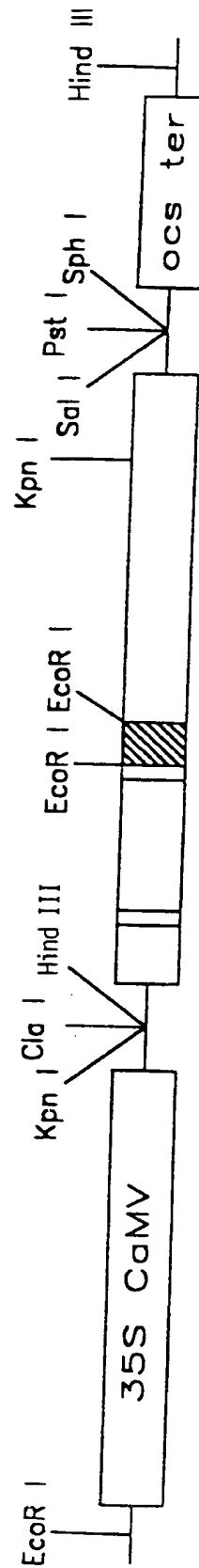
pBin 19 P20 γ ZpBin 19 H30 γ Z

FIGURE 12

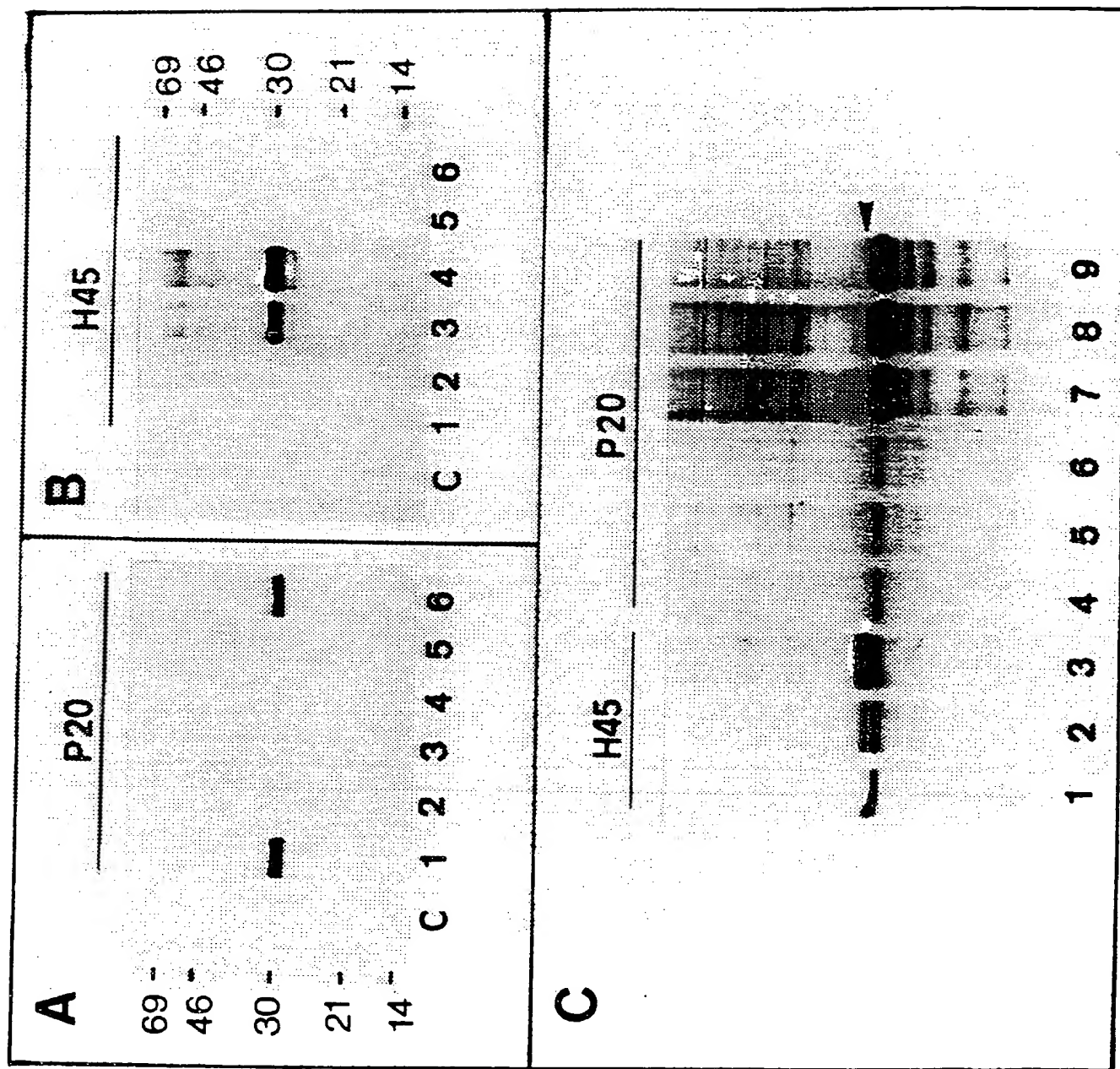


FIGURE 13

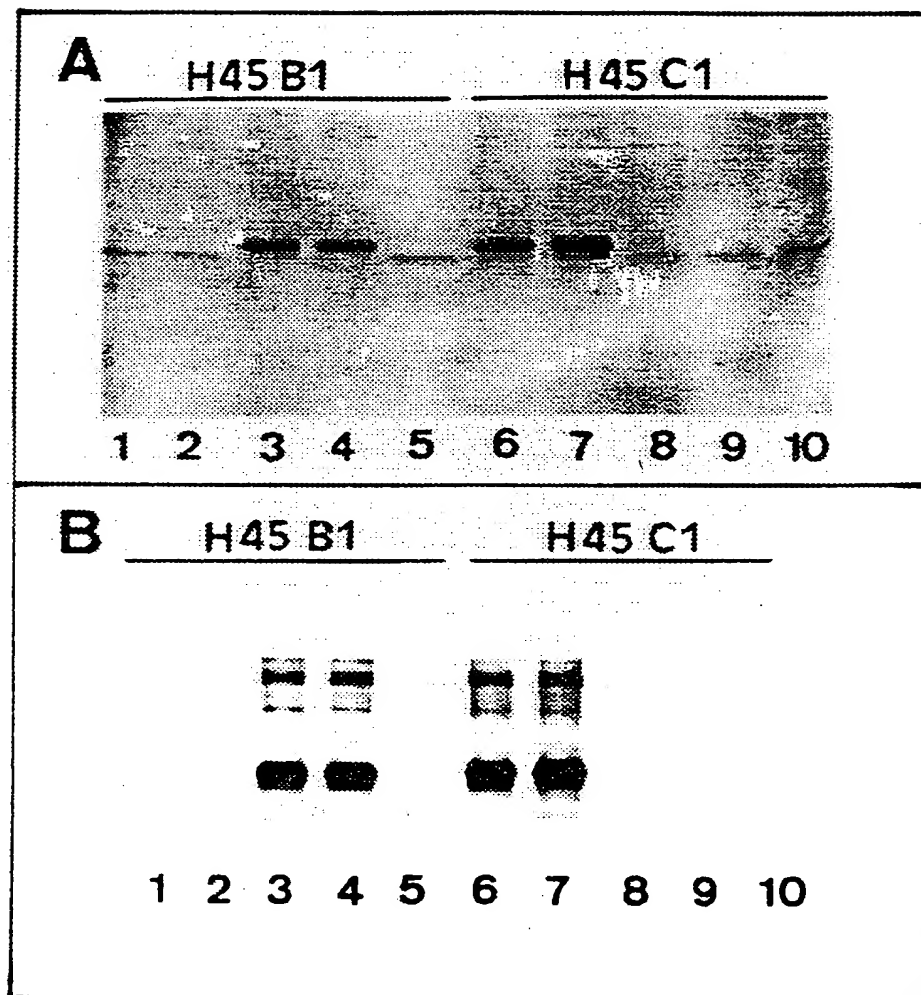


FIGURE 14

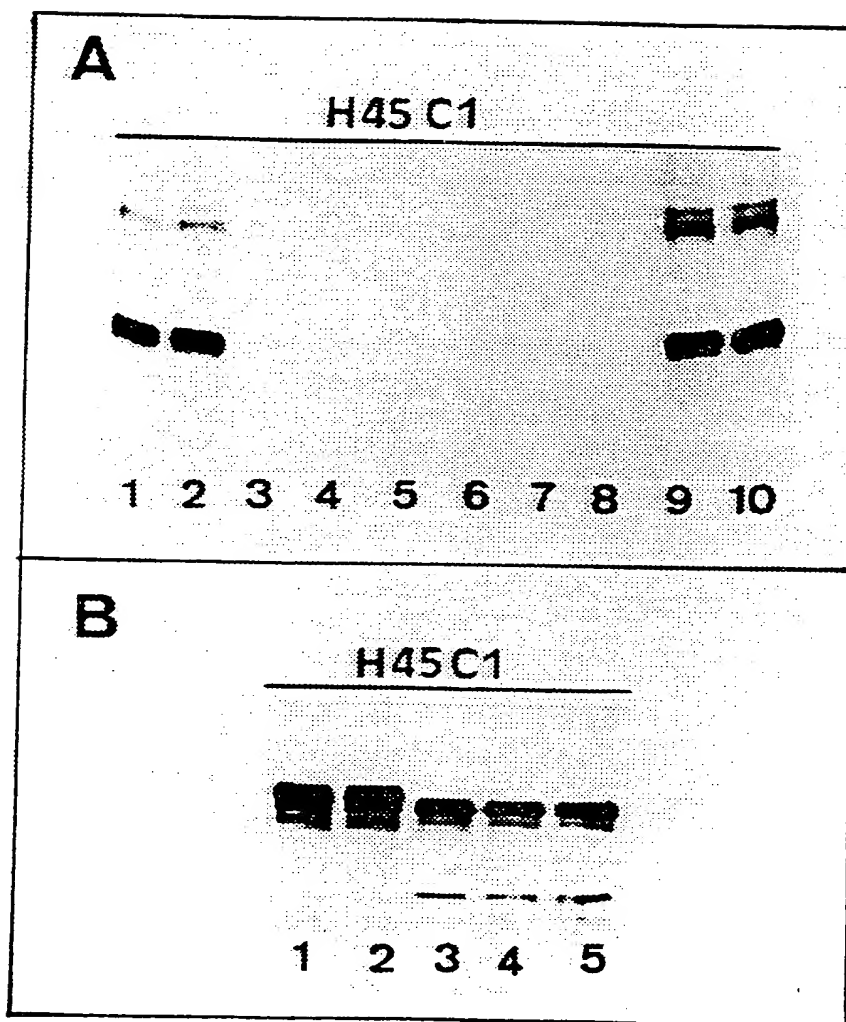


FIGURE 15